

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.

(ii) TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/467,265

(B) FILING DATE: 06-JUN-1995

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ferraro, Gregory D.

(B) REGISTRATION NUMBER: 36,134

(C) REFERENCE/DOCKET NUMBER: 325800-456

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-994-1700

(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 31..843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGGGAACGT GTTCTCTCCCC TCGTTTGGTC ATG GAG GCG CTG CCC CTG CTA GCC	54
Met Glu Ala Leu Pro Leu Leu Ala	
1 5	
GCG ACA ACT CCG GAC CAC GGC CGC CAC CGA AGG CTG CTT CTG CTG CCG	102
Ala Thr Thr Pro Asp His Gly Arg His Arg Arg Leu Leu Leu Leu Pro	
10 15 20	
CTA CTG CTG TTC CTG CTG CCG GCT GGA GCT GTG CAG GGC TGG GAG ACA	150
Leu Leu Leu Phe Leu Leu Pro Ala Gly Ala Val Gln Gly Trp Glu Thr	
25 30 35 40	
GAG GAG AGG CCC CGG ACT CGC GAA GAG GAG TGC CAC TTC TAC GCG GGT	198
Glu Glu Arg Pro Arg Thr Arg Glu Glu Glu Cys His Phe Tyr Ala Gly	
45 50 55	
GGA CAA GTG TAC CCG GGA GAG GCA TCC CGG GTA TCG GTC GCC GAC CAC	246
Gly Gln Val Tyr Pro Gly Glu Ala Ser Arg Val Ser Val Ala Asp His	
60 65 70	
TCC CTG CAC CTA AGC AAA GCG AAG ATT TCC AAG CCA GCG CCC TAC TGG	294
Ser Leu His Leu Ser Lys Ala Lys Ile Ser Lys Pro Ala Pro Tyr Trp	
75 80 85	
GAA GGA ACA GCT GTG ATC GAT GGA GAA TTT AAG GAG CTG AAG TTA ACT	342
Glu Gly Thr Ala Val Ile Asp Gly Glu Phe Lys Glu Leu Lys Leu Thr	
90 95 100	
GAT TAT CGT GGG AAA TAC TTG GTT TTC TTC TTC TAC CCA CTT GAT TTC	390
Asp Tyr Arg Gly Lys Tyr Leu Val Phe Phe Phe Tyr Pro Leu Asp Phe	
105 110 115 120	
ACA TTT GTG TGT CCA ACT GAA ATT ATC GCT TTT GGC GAC AGA CTT GAA	438
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Gly Asp Arg Leu Glu	
125 130 135	
GAA TTC AGA TCT ATA AAT ACT GAA GTG GTA GCA TGC TCT GTT GAT TCA	486
Glu Phe Arg Ser Ile Asn Thr Glu Val Val Ala Cys Ser Val Asp Ser	
140 145 150	
CAG TTT ACC CAT TTG GCC TGG ATT AAT ACC CCT CGA AGA CAA GGA GGA	534
Gln Phe Thr His Leu Ala Trp Ile Asn Thr Pro Arg Arg Gln Gly Gly	
155 160 165	
CTT GGG CCA ATA AGG ATT CCA CTT CTT TCA GAT TTG ACC CAT CAG ATC	582
Leu Gly Pro Ile Arg Ile Pro Leu Leu Ser Asp Leu Thr His Gln Ile	
170 175 180	
TCA AAG GAC TAT GGT GTA TAC CTA GAG GAC TCA GGC CAC ACT CTT AGA	630
Ser Lys Asp Tyr Gly Val Tyr Leu Glu Asp Ser Gly His Thr Leu Arg	
185 190 195 200	
GGT CTC TTC ATT ATT GAT GAC AAA GGA ATC CTA AGA CAA ATT ACT CTG	678
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Leu	
205 210 215	

AAT GAT CTT CCT GTG GGT AGA TCA GTG GAT GAG ACA CTA CGT TTG GTT 726
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 220 225 230
 CAA GCA TTC CAG TAC ACT GAC AAA CAC GGA GAA GTC TGC CCT GCT GGC 774
 Gln Ala Phe Gln Tyr Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 235 240 245
 TGG AAA CCT GGT AGT GAA ACA ATA ATC CCA GAT CCA GCT GGA AAG CTG 822
 Trp Lys Pro Gly Ser Glu Thr Ile Ile Pro Asp Pro Ala Gly Lys Leu
 250 255 260
 AAG TAT TTC GAT AAA CTG AAT TGAGAAATAC TTCTTCAAGT TATGATGCTT 873
 Lys Tyr Phe Asp Lys Leu Asn
 265 270
 GAAAGTTCTC AATAAAGTTC ACGGTTTCAT TACCACAAAA AAAAA 918

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg
 1 5 10 15
 His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala
 20 25 30
 Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu
 35 40 45
 Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala
 50 55 60
 Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys
 65 70 75 80
 Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly
 85 90 95
 Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val
 100 105 110
 Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
 115 120 125
 Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu
 130 135 140
 Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile
 145 150 155 160

Asn	Thr	Pro	Arg	Arg	Gln	Gly	Gly	Leu	Gly	Pro	Ile	Arg	Ile	Pro	Leu	
				165					170					175		
Leu	Ser	Asp	Leu	Thr	His	Gln	Ile	Ser	Lys	Asp	Tyr	Gly	Val	Tyr	Leu	
				180					185					190		
Glu	Asp	Ser	Gly	His	Thr	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	Asp	Lys	
				195					200					205		
Gly	Ile	Leu	Arg	Gln	Ile	Thr	Leu	Asn	Asp	Leu	Pro	Val	Gly	Arg	Ser	
				210					215					220		
Val	Asp	Glu	Thr	Leu	Arg	Leu	Val	Gln	Ala	Phe	Gln	Tyr	Thr	Asp	Lys	
				225					230					235		
His	Gly	Glu	Val	Cys	Pro	Ala	Gly	Trp	Lys	Pro	Gly	Ser	Glu	Thr	Ile	
				245					250					255		
Ile	Pro	Asp	Pro	Ala	Gly	Lys	Leu	Lys	Tyr	Phe	Asp	Lys	Leu	Asn		
				260					265					270		

(2) INFORMATION FOR SEQ ID NO:3:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGGATCC ATGGAGGCGC TGCCCTGCT

29

(2) INFORMATION FOR SEQ ID NO:4:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
    (A) DESCRIPTION: /desc = "PRIMER"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCCATGGA GGCGCTGCCC CTG

23

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCCATGGC TGGAGCTGTG CAGGG

25

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGTCTAGA TCAATTCAGT TTATCGAAAT ACTTCAGC

38

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGGATCC GCTGGAGCTG TGCAGG

26

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGATCCC GAGGCGCTGC CCCTGC

26

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCT CAATTCAGTT TATCGAAATA C

31

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GCGCTGCCC CTG

33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGATCCT CAATTCAGTT TATCGAAATC A

31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGCGGATCC ACCATGGAGG CGCTG

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA ATTCAGTTTA TC

52

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys

1	5	10	15
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser	20	25	30
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe	35	40	45
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu	50	55	60
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser	65	70	75
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly	85	90	95
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile	100	105	110
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg	115	120	125
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val	130	135	140
Asn Asp Pro Pro Cys Cys Arg Ser Val Asp Glu Thr Leu Arg Leu Val	145	150	155
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly	165	170	175
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Pro Lys Thr Lys	180	185	190
Glu Tyr Phe Ser Lys Gln Lys	195		

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Ser Gly Asn Ala Arg Ile Gly Lys Pro Ala Pro Asp Phe Lys	1	5	10	15
Ala Thr Ala Val Val Asp Gly Ala Phe Lys Glu Val Lys Leu Ser Asp	20	25	30	


```

Tyr Lys Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr
   35                               40                               45

Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asn Arg Ala Glu Asp
   50                               55                               60

Phe Arg Lys Leu Gly Cys Glu Val Leu Gly Val Ser Val Asp Ser Gln
   65                               70                               75                               80

Phe Asn His Leu Ala Trp Ile Asn Thr Pro Arg Lys Glu Gly Gly Leu
      85                               90                               95

Gly Pro Leu Asn Ile Pro Leu Leu Gly Asp Val Thr Arg Arg Leu Ser
      100                               105                               110

Glu Asp Tyr Gly Val Leu Lys Thr Asp Glu Gly Ile Ala Tyr Arg Gly
      115                               120                               125

Leu Phe Ile Ile Asp Gly Lys Gly Val Leu Arg Gln Ile Thr Val Asn
      130                               135                               140

Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ala Leu Arg Leu Val Gln
      145                               150                               155                               160

Ala Phe Gln Tyr Thr Asp Glu His Gly Glu Val Cys Pro Ala Gly Trp
      165                               170                               175

Lys Pro Gly Ser Asp Thr Ile Lys Pro Asn Val Asp Asp Ser Lys Glu
      180                               185                               190

Tyr Phe Ser Lys His Asn
      195

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Ala Ala Ala Ala Gly Arg Leu Leu Trp Ser Ser Val Ala Arg Gly
1                               5                               10                               15

Ala Ser Ala Ile Ser Arg Ser Ile Ser Ala Ser Thr Val Leu Arg Pro
      20                               25                               30

Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Ile Leu Trp Ser Ala Ser
      35                               40                               45

Ala Gln Gly Lys Ser Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
      50                               55                               60

```

Ala Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn
65 70 75 80

Gly Glu Phe Lys Glu Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu
85 90 95

Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu
100 105 110

Ile Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys
115 120 125

Glu Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp
130 135 140

Ile Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Thr
145 150 155 160

Leu Leu Ser Asp Ile Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu
165 170 175

Leu Glu Ser Ala Gly Ile Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro
180 185 190

Asn Gly Val Val Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg
195 200 205

Ser Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Phe Val Glu
210 215 220

Thr His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Glu Ser Pro Thr
225 230 235 240

Ile Lys Pro Ser Pro Thr Ala Ser Lys Glu Tyr Phe Glu Lys Val His
245 250 255

Gln

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ser Ser Gly Asn Ala Lys Ile Gly Tyr Pro Ala Pro Asn Phe Lys
1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser

20					25					30					
Glu	Tyr	Lys	Gly	Lys	Tyr	Val	Val	Phe	Phe	Phe	Tyr	Pro	Leu	Asp	Phe
		35					40					45			
Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	Ile	Ala	Phe	Ser	Asp	Arg	Ala	Asp
	50					55					60				
Glu	Phe	Lys	Lys	Leu	Asn	Cys	Gln	Val	Ile	Gly	Ala	Ser	Val	Asp	Ser
65					70					75					80
His	Phe	Cys	His	Leu	Ala	Trp	Ile	Asn	Thr	Pro	Lys	Lys	Gln	Gly	Gly
				85					90					95	
Leu	Gly	Pro	Met	Asn	Ile	Pro	Leu	Ile	Ser	Asp	Pro	Lys	Arg	Thr	Ile
			100					105					110		
Ala	Gln	Asp	Tyr	Gly	Val	Leu	Lys	Ala	Asp	Glu	Gly	Ile	Ser	Phe	Arg
		115					120					125			
Gly	Leu	Phe	Ile	Ile	Asp	Asp	Lys	Gly	Ile	Leu	Arg	Gln	Ile	Thr	Ile
	130					135					140				
Asn	Asp	Leu	Pro	Val	Gly	Arg	Ser	Val	Asp	Glu	Ile	Ile	Arg	Leu	Val
145					150					155					160
Gln	Ala	Phe	Gln	Phe	Thr	Asp	Lys	His	Gly	Glu	Val	Cys	Pro	Ala	Gly
				165					170					175	
Trp	Lys	Pro	Gly	Ser	Asp	Thr	Ile	Lys	Pro	Asp	Val	Asn	Lys	Ser	Lys
			180					185					190		
Glu	Tyr	Phe	Ser	Lys	Gln	Lys									
			195												